SEARCH REQUEST FORM

Scientific and Technical Information Center

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Art Unit: Phone Number 30	Serial Number:							
Requester's Full Name: Art Unit: Phone Number 30 Mail Box and Bldg/Room Location: F	Results Format Preferred (circle):	PAPER I	DISK E-MAIL					
If mor than one search is submitted, please prior			*****					
Please provide a detailed statement of the search topic, and descr Include the elected species or structures, keywords, synonyms, a utility of the invention. Define any terms that may have a specia known. Please attach a copy of the cover sheet, pertinent claims,	cronyms, and registry numbers, and co I meaning. Give examples or relevant	mbine with t	he concent or					
Title of Invention:								
Inventors (please provide full names):								
Earliest Priority Filing Date:								
For Sequence Searches Only Please include all pertinent informati appropriate serial number.	•	tent numbers)	along with the					

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
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STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher:	NA Sequence (#)	STN
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Searcher Location:	Structure (#)	Questel/Orbit
Date Searcher Picked Up:	Bibliographic	Dr.Link
Date Completed: YII (UZ	Litigation	Lexis/Nexis
Searcher Prep & Review Time:	Fulltext	Sequence Systems
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P Qy	Ma Oy Db	D Qu	A; State A; Mole A; Resi A; Cros A; Note	A; Ti	A;Re A;Cr R;Ha felt	A; Ac A; St A; Mo	A;Ti A;Re	A; Ke R; Cr	A; Ac A; St	A; Ti	R; Ly	RESU I384 flt3 C;Sp C;Da		
61	ट्	ery Ma	us:	Title: I	sidues oss-re nnum, A.;	cessic atus: lecule	gene I	man, S	;Accession: ;Status: pro; ;Molecule t	Title: C	man, s	RESULT 1 138440 flt3 ligand C; Species: C; Date: 29-		44444333333333333333333333333333333333
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SNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPS 	SSDFA	3 DB 2; Leng 8e-99;	.83844; PIDN:AAA17999.1;	r tyrosine kinase regul 5428	2036; PIDN:AAA90949 McClanahan, T.; 2 A, R.; Rennick, D.;	m GB/EMBL/DDBJ	and murine flt3 ligand 2581	g494978; PIDN:AAA19825: B.; Fletcher, F.; John	m GB/EMBL/DDBJ	ue of the murine flt3 l 5842	; Brasel, K.; de Vries,	n 29-may-1998 #text_change	ALIGNMENTS	
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C;Species: Homo sapiens (man, C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #tex C;Date: 20-Oct-1995 #tex C;Date: 20-Oct-1
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A; Introns:
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C;Date: 29-May-1998
C;Accession: I39076
                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-178 <R
                                                                                                                                                                                                                                                                           A; Title: Structural analysis of human and murine flt3 A; Reference number: I39075; MUID:96032581 A; Accession: I39076
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Oncogene 11, 1165-1172, 1995
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A; Note: the authors translated
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Best Local Similarity
Matches 160: Component
                                                                                                                                                  Genetics:
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0; Mismatches 0;
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Pred. No. 8.5e-67;
7; Mismatches 27
                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
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                                                       Length 178;
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       Gaps
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M.G.; Zlotnik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.G.;
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120 61

LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT 177 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT

120

60 59

60

1 MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT

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A; Nolecule type: DNA
A; Residues: 1-197, 'L',198-231 <RE2>
A; Residues: 1-197, 'L',198-231 <RE2>
A; Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
R; Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazifelt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.
felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick D.; Roncarolo, M.G.
Nature 368, 643-648, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
A49265
A49265
(C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C:Accession: A49265; 149347; 149346; S43290
R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries,
D.; Williams, D.E.; Beckmann, M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L23636; NID:g439441; PIDN:AAA39436.1; PID:g439442 R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Esconcogene 11, 1165-1172, 1995 A;Title: Structural analysis of human and murine flt3 ligand genomic loc: A;Reference number: 139075; MUID:96032581 A;Accession: 149347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell 75, 1157-1167, 1993
A;Title: Molecular cloning of a ligand for A;Reference number: A49265; MUID:94084791
A;Accession: A49265
                                                                                                                                                                                                                                                                                                         Nature 368, 643-648, 1994. A. AMERICA, D.; KONCAROLO, M.G.; ZIOTNIK A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi A;Reference number: S43290; MUID:94195428
A;Accession: S43290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-163,'G',165,'HYAG' <RES>
A;Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1;
A;Accession: I49346
                                                                                                                        A; Introns: 11/3; 49/3; 67/3; 115/3; C; Keywords: transmembrane protein
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Query Match
Best Local Similarity
Matches 163; Conserv
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       Conservative
                             61.9%;
70.3%;
       17;
    Score 768.5; DB 2
Pred. No. 1.3e-58;
7; Mismatches 43
                                                                                                                                              164/1;
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                                                   Length
       Indels
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                                                                                                                                                                                          Fig.
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                                                                                                                                                                                                                                                                                                                                                                                                           Zlotnik
                                                                                                                                                                                                                                                                                                                                                                                                                                      J.F.;
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C;Species: Mus sp. (mouse)
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I58343
R;Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Oncogene 10, 149-157, 1995
A;Title: Identification of soluble and membrane-bound isoforms of the murine A;Reference number: I58343; MUID:95124710
A;Accession: I58343
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-220 <RES>
A;Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1; PID:g913480
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A;Molecule type: mRNA
A;Residues: 1-220 <HAN>
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R:Hannum, C:; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; felt, A:, Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, Nature 368, 643-648, 1994
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Best Local
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                                                                                                                                    MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LREVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATRLTATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELPEPRPRQLLLLLLLLLLVLLAAAWGLRWQRARRR----GELHPGVPLP 228
                                  VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APTAPQPP--LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MINITED TO THE TRANSPORT OF THE PROPERTY OF TH
                                                                                                 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
   Similarity
                                                                                                                                                                                                                                         Conservative
mouse
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61.5%;
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 606.5; DB 2
Pred. No. 9.4e-45;
                                                                                                                                                                                                                                                                  Score 606.5; DB 2
Pred. No. 9.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                     рв 2;
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                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                               Gaps
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M.G.; Zlotnik,
                                                                                                                                                                                                                                  5
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J. Gen. Virol. 67, 1759-1816, 1986

J. H. Virol. 67, 1759-1816, 1986

A; Title: The complete DNA sequence of varicella-zoster virus
A; Reference number: A27345; MUID:86306657

A; Accession: C27342

A; Molecula ***---
                                                                                                        C;Superfamily: herpesvirus 77K alpha trans-inducing protein C;Keywords: trans-inducing protein; transcription regulation
                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-661 <DAV>
                                                                                                                                                                                                                                                                                                                                                               74K alpha trans-inducing protein - human herpesvirus 3 C;Species: human herpesvirus 3, varicella-zoster virus C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #tey C;Accession: C27342
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
TNBE12
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A; Introns: 742/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data A; Reference number: 219597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F54F12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change C;Accession: T22672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
T22672
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                                                                                                                                                     A; Gene:
                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                               A;Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27895.1; PID:g60001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z81548; NID:e1062020; PIDN:CAB04464.1; GSPDB:GN00021; CESP:FA;Experimental source: clone F54F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1217 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Barlow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:F54F12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T22672
Query Match 7.4
Best Local Similarity 26.6
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 MERLKTVAGSKMQGL---LERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPVGLLLLAA----AWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALKPWITRQNFSRCLELQCQPDSSTL---PPPWSPRPLEATAPTAP-----QPPLLLLLL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATRLTATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LEATAPTAPQPPLLL-----LLLLPVGLLLLAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL----FFASYASNLA 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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23.6%;
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                      7.48;
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3;
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    Score 92; DB 1; Length 661;
Pred. No. 3.8;
29; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 93; DB 2; Length 1217; Pred. No. 6.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          30-Sep-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1024/2; 1102/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          16-Jul-1999
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29;

36;

11;

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adhalin - golden hamster
(;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996
C;Accession: I48201
R;Roberds, &.L.; Campbell, K.P.
FEBS Lett. 364, 245-249, 1995
A;Titie: Adhalin mRNA and cDNA sequence are normal
A;Reference number: I48201; MUID:95278335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: clone C; Genetics:
A; Gene: CESP: C28D4.2
A; Map position: 4
A; Introns: 26/3; 72/3; 118/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library A; Reference number: Z19139
A; Accession: T19543
A; Status: preliminary; translated A; Molecule type: DNA
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T19543
T19543
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to
C;Accession: T19543
R;MCMurray, A.
                                                                                                                                      RESULT
I48201
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Best Local :
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                                                                                                                                                                                                                                       230 LLLVE 234
                                                                                                                                                                                                                                                                          223
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                                                                                                                                                                                                        ITVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                             VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLR-FVQTNISRLLQET- 134
                                                                                                                                                                                                                                                                        PKEPO
                                                                                                                                                                                                                                                                                                      PTAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTP---RPGE----QVPPVPSPQD
                                                                                                                                                                                                                                                                                                                                      VFTLLSERNLGPKMLGVFPGGRFEQFIPSRALQCLEISKPGLSKLIAPIVARVHTLDAPI 222
                                                                                                                                                                                                                                                                                                                                                                                                        VKIEEF--RIRAITGG-MSNLLFLVELPAH-LTPIQMEPEKALLRVHCQSDIDQLLSESV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTDCVDLKKVFSKFDSSAPISGEILFRARFLCAKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDYPVTVASNLQDEELCGGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYGWMLWFLDVVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSDYRGICQELREALGAVQKYM---YFMR-----PDDPTNPSPDTRIRVQEIAAYTAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSP-RPLEATAPTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLW-WVYENTYWQYLKYTTGAEVPVTSEKVNKKSKSTVLLFSSVVANKPISRHPFKSKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLWRLVLAQRWMERLKTVAGSKMQGLLERVN----TETHFVTKCAFQP---PPSCLRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTSPVLQSTERHSVLLGLHHNNVPESLVVSCMSNDVHDGFMQRYMETIQRCLDDLKLSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLSSGLSGTQDCS----FQHSPISSDFAVKI--RELSDYLLQDYPVTVASNLQDEELCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                          271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: Z82259; PIDN: CAB05129.1; 
>e: clone C28D4
                                                                                                                                                                                                                                                                                                                                                                         SEQLVALKPWITRQNFSRCLELQC----QPDSSTLPPPWSPR--PLEATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.2%;
24.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 89.5; D
Pred. No. 4.2;
29; Mismatches
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                   in
                                                                                    #text_change
                   the
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                   cardiomyopathic hamster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GGAWRK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75;
                                                                                    20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342/2;
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A;Gene: GDB:SF3A120; PRP21; SAP114
A;Cross references: GDB:9955873
A;Map position: 22q12.1-22qter
C;Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology C;Keywords: pre-mRNA splicing
C;Keywords: pre-mRNA splicing
F;714-790/Domain: ubiquitin homology <UBH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: I48201
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1;
C;Superfamily: mouse adhalin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicing factor SF3a 120K chain - human C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S60735; S60733
Q
                                  B
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                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 51-62;82-94;270-275;397-414;448-463
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-793 <KRA>
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                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                          A; Accession: S60733
                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                       A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S60735
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA 1, 260-272,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Kraemer, A.; Mulhauser, F.; Wersig, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S60735
                                                                                         Query Match
Best Local Similarity
Matches 67; Conser
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Best Local Similarity
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   64
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                                                                LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATSDIQMVHHCTIHGNTEELRQMAARREVPRPLSTLPMFNVRTGERLPPRVDSAQVPLI
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                                    LPPAPAPDEYLV:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGLWRL-----VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTRQRLLLLI-----EDPEGPRLPYQAEFLVRSHDVEEVL----PSTPANRFL--TAL 161
   LQDEELCGGLWRLVLAQRWME-RLKTV-
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                                                                                                  Conservative
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                                                                                                             7.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     factor SF3a120
MUID:96079958
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                                                                                                34;
                                                                                                Score 89; DB
Pred. No. 8.4;
84; Mismatches
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Pred.
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                                    SPITGE - - - KI - -
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3.7;
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                                                                                                  79;
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   -AGSKMQGLLERVNTEIHE 107
                                                                                                                                Length
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                                                                                                                                 793
                                                                                                  120;
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                                                                                                                                                                                                                                                                                                                                         PID:g899298
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                                 ---PASK 424
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OP protein - Kennedya yellow mosaic virus (;Species: Kennedya yellow mosaic virus C;Species: Kennedya yellow mosaic virus C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999 C;Accession: JQ0532 R.Ding, S.; Keese, P.; Gibbs, A. J. Gen. virol. 71, 925-931, 1990 A;Title: The nucleotide sequence of the genomic RNA of kennedya yellow mosai A;Reference number: JQ0532; MUID:90218040 A;Accession: JQ0532; MUID:90218040 A;Accession: JQ0532 A;Molecule type: mRNA A;Residues: 1-753 CDIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein KIAA0476 - human C;Species: Homo sapiens (man) C;Deecies: Homo sapiens (man) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000 C;Accession: T00257
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A; Residues: 1-1386 <SEK>
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A;Tille: Characterization of cDNA clones in size-fractionated cDNA libraries A;Reference number: Z14085; MUID:98116662
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A;Cross-references: GB:D00637; NID:g221969; PIDN:BAA00531.1; A;Experimental source: strain Jervis Bay isolate
                                                                                                                                                                                                                                                                                                                                                                                                              망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BAA32321.1;
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Best Local Similarity
Matches 53; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGASGSKDAPVPGGP------GPVLSDRRLCLA--LDEPQLCNGHMGGASRR 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPRPPMASVVRLPPGSVIAPMPPIIHAPRINVVPMPPSAPPIMAPRPPPMIVPTAFVPAP 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APQPPLLLLLLPVGLLLLAAAWCLHWQRTR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEETAIGKKIGEEEIQKPEEKVTWDGHSGSMARTQQAAQANIT--LQEQIEAIHKAKGLV 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VESGAWAYLSPLVLRKELESLVENEGSEV-----LALPELPSAHPIIFWNLLWYFQRL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TRONF--SRCLELOCOP------DSSTLP-----PPWSPRPLEAT----APT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTKCA-----FQPPPSCLRF-------VQTNISRLLQETSEQLVALKPWI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLVALKPWITRQNFSRCLELQCQ-PDSSTLPPPW-SPRPLEA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC----GGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEDDTKEKIGPSKPNEIPQQPPPPSSATNIPSSAPPITSVPRPPTMPPPVRTTVVSAVPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1%; Score 88.5; 1
23.1%; Pred. No. 17;
ative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              WRVHSQ-IPQRVVWPG----PVPASLSLALLE 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CDGPSHSQAPSPWLTPDPASVQVRLLWDVLTPDPNSCPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1386;
                                                                                                                                         kennedya yellow mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TAPTAPQPP 185
                      PID:d1000986; PID:g221970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:g3413914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly C;Species: Drosophila melanogaster C;Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999 C;Accession: A32290; S12008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
A32290
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A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-227, 'A', 229-479 <JIM>
A; Cross-references: EMBL: X57495; NID: g7706; PIDN: CAA40732.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Complementation of fission yeast cdc2(ts) A; Reference number: S12008; MUID:91006056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Jimenez, J.; Alphey, L.; EMBO J. 9, 3565-3571, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; R;Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 57, 177-187, 1989
A;Title: Genetic control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Edgar, B.A.;
Cell 57, 177-1
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В
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A; Accession: A32290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 RVNTEIHFVTKCAFQPPPSCLRF----VQTNIS-----RLLQETSEQLVALKPWITR 147
                                         118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227
147
                                                                                    118 CSMESSMDDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 22.3 hes 41; Conservative
                                                                                                                             58
                                                                                                                                                                         72
                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                1 MTVLAPAWSPTTYLLL---LLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNFSR----CLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLP------ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPDVFHDCQPSSPTSHVVGYRRLLGSGISLPFKLAFW-----RRRSPNPARHLPPPPP 586
                                                                                                                                                                      MGLLSPEGSPQRFQIVRQPKILPAMGVSS------DHTPARS-FRI-FNSLSS-----T 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNLRRHSALPLLLPIHPTKTTQPHPAVPQP--TAGPTPHPPPTKKIPLHPPKSQERHPSP 533
                                    SCLREVQTNISRLLQETSEQLVALKP---WITRQNESRCLEL-QCQPDSSTLPPPWSPRP 173
                                                                                                                      VTVASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP 117
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase:FBgn0003525
-SLISGQIKEQPAAKSPAGLSMRRPSVRRCLSMTESNTNSTTTPPPKTPE-
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22.3%;
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22.9%;
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Pred. No. 9.6;
                                                                                                                                                                                                                                                         Score 87.5; D
Pred. No. 6.3;
84; Mismatches
                                                                                  ·YMELFEMESQSQ.
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                                                                                                                                                                                                                                                                                                         DВ
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                                                                                    --QTALGE-----P
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                                                                                                                                                                                                                                                             79;
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199
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A;Gene: Ptk-3
A;Gene: Ptk-3
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-terminal homology <DN1>
F;31-186/Domain: discoidin I amino-terminal homology <DN1>
F;605-909/Domain: protein kinase homology <KIN>
F;613-621/Region: protein kinase ATP-binding motif
Search completed: April 1, 2002, 06:15:21 Job time: 87 sec
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A;Title: Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of Ptk A;Reference number: A53137; MUID:94173920
A;Accession: A53137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: A53137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-910 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.0%; Score 87; DB 2; Length 910; Best Local Similarity 24.5%; Pred. No. 15; Matches 38; Conservative 12; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                             143 PWITRQNFSRCLELQCQPDSSTLPP-PW---SPRPLEATA----PTAPQP------ 184
                                                                                                                                                  471 NRPGPREPPPYQEPRPRGTPTHSAPCVPNGSALLL 505
                                                                                                                                                                                                          415 ILIGCLVAIILLLLIIALML----WRLHWRRLLSKAERRVLEEELTVHLSVPGDTILIN 470
                                                                                                                                                                                                                                                                                                                          185 -----PLLLLLLPVGLLLLAAAWCLHWQR----TRRR------
                                                                                                                                                                                                                                                                                                                                                                                     356 PWLLESEISFISDV-VNDSSDTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTA 414
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243 VTISH 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 LEATAPTA---PQPPLLLLLLLEVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDL 230
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Perfect score:
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1 MTVLAPAWSPTTYL
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Gapop 10.0 , Gapext 0.5
                                            100059 seqs, 36664827 residues
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124.927 Million cell updates/sec
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB Maximum DB

seg length: 0 seg length: 2000000000

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	score	Query Match	Length	DB	ID	Description
, _	124	000	235	٠,	FL3L_HUMAN	771 homo
u N	768	61.8	232	4 د	FL3L_MOUSE	72 mus mus
. د	ی د	۰ د 4 د	561	ب د	ATIZ_VZVD	4- 0
4.1	89.5	7.2	94	ب.	GBR2_HUMAN	9
· Uī	89	7.2	387	_	SGCA_MESAU	5 meso
6	8	7.2	793	_	S3A1_HUMAN	9
7	87.5	7.0	415	-	TNRC_MOUSE	4 mus
8	7.	7.0	479		MPIP_DROME	P20483 drosophila
9	87	7.0	910	ب	DDR1_RAT	4
10	œ	7.0	911	_	DDR1_MOUSE	σ
11			1394	щ	CNG4_BOVIN	sod
12	86		485	<u>بــ</u>	SSGP_VOLCA	
13			282	Ц	ATF5_HUMAN	Q9y2d1 homo sapien
14	85		366	_	FCGN_RAT	rattu
. 15			582	ب.	MNT_HUMAN	homo
, ,	, α		/32	-	YE'48_HUMAN	nomo
17			671	ب.		7 homo
18	83		758	ب ،	VKGC_HUMAN	5 homo
19	81.5		488	بر	MM11_HUMAN	homo
20	81.5		591	دسو	MNT_MOUSE	9 mus m
21	81.5		2124	ب	Y192_HUMAN	homo
22	81		283	L	ATF5_MOUSE	1 mus m
23	81		387	_	SGCA_MOUSE	P82350 mus musculu
24	81		428	_	EPC_HUMAN	homo
25	8		1248	_	DIA1_HUMAN	homo
26	80.5	6.5	1402	ш	IF4G_RABIT	oryct
27		6.4	397	_	CEFD_STRCL	9
28	90	6.4	940	ш	GBR2_RAT	71
29		6.4	1174	ᆫ	KPC1_COCHE	N
30		6.4	1794	Ь	YAV1_SCHPO	72
31	79	6.4	805	ᆫ	YGW6_YEAST	P53086 saccharomyc
32	•	6.3	251	ᆫ	HXB4_HUMAN	ω
33	8	6.3	382	۳	AVRB_RAT	Çī

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ALIGNMENTS

RESULT 1 FL3L_HUMAN

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and this statement is not removed.	88
European Bioinformatics Institute. There are no re	388
This SWISS-PROT entry is copyright. It is produced through a collaborat hetween the Swiss Institute of Bioinformating and the EMRI outstation	38
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SPLICING.	3 8
	3 6
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM	36
FACTORS AND INTERLEUKINS.	6
\rightarrow	င္ပ
-!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC	6
rigand genomic roci.	RL 7
analysis of human and murino fl+3 ligand	Z Z
Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,	RA
32581; PubMed=7566977;	RX
[3]. SEOUENCE FROM N.A., AND ALTERNATIVE SPLICING.	R R
2	7 7
tactor for early hematopoietic progenitor cells.";	7 Z
"Cloning of the human homologue of the murine flt3 ligand: a growth	감
Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.;	RA
L., Johnson L	RA
9	RX
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hapmatonojetic stem cells and is encoded by variant RNAs ":	ξ. 1
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Celner G., Namikawa R., Rennick D., Ronca	RA
N., Peterson D., Menon S., Shanafelt A.,	RA
., Wagner J., Mattso	RA
Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,	RA
	RX
SEQUENCE FROM N.A.	R R
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ia; Primates;	28
; Metazoa; Chordata; Craniata; Vertebrata; E	8
piens (Human)	SO
FLT3LG.	GN
	D C
SI CYTOKINE PRECURSOR (FMS-RELATED TYROSINE KINASE 3 LIGAND) (FIT3	7 5
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	AC I
FL3L HUMAN STANDARD; PRT; 235 AA.	ID
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RESULT
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01-OCT-1996
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Lyman S.D., James L., Vandenbos T., Devries Gliniak B., Hollingsworth L.T., Ficha K.S., Splett R.R., Fletcher F.A., Maraskovsky E.,
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TRANSMEM
                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-94195428; PubMed-8145851;

Hannum C., Culpepper J., Campbell D., McClanahan T., Zura

Hannum C., Kastelein R., Hudak S., Wagner J., Mattson J.

Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,

Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo

Zlotnik A., Rosnet O., Dubreuil P., Birnbam D., Lee F.;

"Ligand for FLT3/FLK2 receptor tyrosine kinase regulates
haematopoietic stem cells and is encoded by variant RNAS.

Nature 368:643-648(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 2
MOUSE
                                                              STRAIN=SJL/J;
MEDLINE 94084791;
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Mammalia; Eutheria;
                                                                                                        SEQUENCE FROM N.A.
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P49772;
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; U03858; AAA19825.1;
; U29874; AAA90949.1;
; U29874; AAA90950.1;
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(Rel. 40,
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Rodentia;
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Last annotation update)
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N-LINKED (GLCNAC. . .) (POTENTIAL).

VLINKED (GLCNAC. . .) (POTENTIAL).

DSSTLPPPMSPRPLEATA -> VETVPHRVSQDGLDLLTS
(IN SOLUBLE ISOFORM).

MISSING (IN SOLUBLE ISOFORM).

G -> A (IN REF. 1).

MW; 73B95BF693B4CECF CRC64;
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    ; P., Bras
, McKenna
, Farrah T
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                    Brasel K.
(enna_H.J.,
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; Murinae; Mus
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MEDLINE=96032581; Pt
MEDLINE=96032581; Pt
Lyman S.D., Stocking
Escobar S.:
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EMBL; L23636; AAA39436.1; -
EMBL; U29875; AAA90951.1; -
EMBL; U29875; AAA90952.1; -
EMBL; S76459; AAB33069.1; -
EMBL; S76451; AAB33070.1; -
EMBL; S76461; AAB33077.1; -
EMBL; U44024; AAA93307.1; -
EMBL; U44024; AAA93306.1; -
EMBL; U44024; AAA93306.1; -
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or send a
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-- FONCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATE FACTORS AND INTERLEUKINS.
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MEDLINE=95124710;
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                                                                                                                                       VARSPLIC
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11:1165-1172(1995).
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ligand for the flt3/flk-2 tyrosine kinase
ve factor for primitive hematopoietic cell
                                                                                                                                                                                                                                                                    Transmembrane; Alternative
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SL CYTOKINE.
SL CYTOKINE.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
DSSTLLPPRSPTALEAMELPEPRPRQLLLLLLLLLPLTIVL
LAAANGLRWORARRGELHPGVPLPSHP -> GNGGPRAQH
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        DSSTLL -> GSHYAG (IN ISOFOM E6).
MISSING (IN ISOFOM E6).
A -> G (IN REF. 1).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
                                                                                          LKMYLYV (IN ISOFORM 5H)
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STEP TO THE TET THE TET THE TET TO COLOR OF THE TET TH

Query Match Best Local Sir Matches 163;

Similarity

61.8%; 70.0%;

Score Pred.

768;

DB 1; .9e-58;

Length 232;

Indels

10;

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Conservative

17;

Mismatches

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P09264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Varicella-zoster virus (strain Viruses; dsDNA viruses, no RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-86306657; PubMed-3018124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alphaherpesvirinae;
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01-NOV-1990
                                                                                                                                                                                                                                                                    Transcription regulation; SEQUENCE 661 AA; 74272
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e complete DNA sequence of varicella-zoster virus.
Gen. Virol. 67:1759-1815(1986).
FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DE
ACTIVATION OF ALPHA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR-1989 (Rel. 10,
AR-1989 (Rel. 10,
OV-1990 (Rel. 16,
A TRANS-INDUCING F
 GYGWMLWFLDVVD----
                                                               GLW-WVYENTYWQYLKYTTGAEVPVTSEKVNKKSKSTVLLFSSVVANKPISRHPFKSKVI
                                                                                                                          GLWRLVLAQRWMERLKTVAGSKMQGLLERVN----TEIHFVTKCAFQP---PPSCLRFV
                                                                                                                                                                           LLSSGLSGTQDCS----FQHSPISSDFAVKI--RELSDYLLQDYPVTVASNLQDEELCG-
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                       QPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLL
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                                                  NSDYRGICQELREALGAVQKYM---YFMR-----
                                                                                                                                                                                                    1 Similarity 26.6 61; Conservative
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                                                                                                                                                                                                                                                                                                                                and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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Varicellovirus
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, Last annotation update)
FACTOR 74 KDA PROTEIN.
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ARVCRHLKLQFRRIRGPRASV----IPDDLL
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Pred. No.
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Stage;
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075899; 075974; 075975; Q9UNS9; Q9UNR1; Q9P1R2;

20-AUG-2001 (Rel. 40, Created)

20-AUG-2001 (Rel. 40, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-F
RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2) (G PROTEIN-COUPLED RECEPTOR

51) (GPR 51) (HG20).
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proximal to t
chromosome 9.
RIA-R2 INTERACTION.

MEDLLINE=99175124; PubMed=10075644;

Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan Rargman S., Chateauneuf A., Tsukamoto N., McDonald T., Whiting P., Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F., Bonner T.I., O'Neill G.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20193514; PubMed=10727622; Clark J.A., Mezey E., Lam A.S., Bonner T.I.; "Distribution of the GABA(B) receptor subunit Brain Res. 860:41-52(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Heterodimerization is required GABA(B) receptor.";
Nature 396:679-682(1998).
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                                                                                                                                                                                                                                                   expression
GABABR1.";
                                                                                                                                                                                                                                                                                                         MEDLINE=99263199; PubMed=10328880;
Martin S.C., Russek S.J., Farb D.H.;
"Molecular identification of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'Neill G.P.,
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Borowsky B., Laz T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herzog H.;
"Cloning and characterization of a novel human "Cloning and characterization of a novel human for GABA and low affinity for GABA and low 
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TISSUE=Cerebellum;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chateauneuf
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MEDLINE=99189236; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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ld T., Bonnert T.,
oulombe N., Kargman
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Primates;
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n S., Caskey T., Evans
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receptor 4 supports receptor.";
J. Pharmacol. Exp. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R1A-R2 INTERACTION MEDLINE=20237752; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a GABAB receptor subunit, gb2, required functional GABAB receptor activity.";
J. Biol. Chem. 274:7607-7610(1999).
                                                                                                                                                                                                                                                                 HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT INVARIANT RECTIFYING POTASSIUM (KIR) LOUNDUCTANCE THAT UNDERLIES THE LATE INHIBITORY POSTSYNAPTIC POTENTIALS, NOT ONLY IMPLICATED IN SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pharmacol. Exp. Ther. 293:460-467(2000).

FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENVLYL CYCLASE ACTIVITY STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE TIME-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
PLASMA MEMBRANE.
ALTERNATIVE PRODUCTS:
                                                     SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MCCOEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-E
                                                                                                                                                                           SUBUNIT: HETE
IS EFFECTIVE
                                                                                                                                                                                                                                          POTENTIATION, SI
ANTINOCICEPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
                                                                                                                                                     HAPPEN
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                                                                                                                                                                              HETERODIMER OF
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CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND TEMPORAL LOBE, OCCIPITAL POLE AND CEREBLLIUM, FOLLOWED BY CORPUS CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, ANYGDALA AND MEDULLA.

WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.

DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

GABA-B RECEPTOR SUBFAMILY.

PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, E.

ISOFORMS; SPLICING.

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an email to license@isb-sib.ch). (See

PRINTS; F PRINTS; F PRINTS; F PROSITE; Pfam; PI PRINTS; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; InterPro; IPR001828; InterPro; IPR000337; or send use by non-profit institutions as long a modified and this statement is not removed. Pfam; EMBL; ; AJ012188; CAA09942.1; AF055085; AAC63228.1; AF095723; AAC63383.1; AF095724; AAC63384.1; AF095724; AAC63384.1; AAC63384.1; AAC63384.1; AAC63384.1; AAC63386.1; AAC63336.1; AAC69345.1; AAC69755; AAC69345.1; AAC69755; AAC69345.1; AAC69755; AAC69345.1; AAC69345.1; AAC69755; AAC699345.1; AAC699945.1; AAC699945.1; AAC699955.1; AAC699955.1; AAC699955.1; AAC699955.1; AAC699955.1; AAC PF01094; ANF_receptor; 1. AF099033; PRO0248; (PR01176; (PR01177; (PR01178; (PR50099; E; PS500979; AAC99345.1; AAD45867.1; GABAB2RECPTR.
; PRO_RICH; 1.
; G_PROTEIN_RECEP_F3_1; FALSE_NEG GABABRECEPTR. GABAB1RECPTR. GPCRMGR ; ANF_recept ; GPCR_Mgr. _receptor

Sakamoto Masaki T.

o A., o... T., Toyo-oka

MEDLINE=98054328; PubMed=9391120;

TISSUE=Heart muscle;

Ono K.,

Abe M.,

Jasmin

G.,

Eki

Τ.,

Murakami Y.,

Hanaoka

SEQUENCE FROM N.A STRAIN-SYRIAN; TI

NCBI_TaxID=10036; Mesocricetus Mammalia; Eutheria;

Eukaryota;

Metazoa;

Rodentia; Chordata;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Cricetinae;

Mesocricetus

auratus

(Golden hamster)

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RESULT 5
SGCA_MU ID SGCA_MU ID SGCA_MU ID SGCA_MU ID AC 20-AUG DT 20-AUG DT 20-AUG DE ALPHA-DE ASSOCIGA SGCA...
OS MESOCIGA SGCA...
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PS00981; G_PROTEIN_RECEP_F3_4; 1.
PS50259; G_PROTEIN_RECEP_F3_4; 1.
n coupled receptor; Transmembrane; Glycoprotein; Signal; ptic membrane; Coiled coil; Alternative splicing;
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S -> R (IN REF. 5).
P -> R (IN REF. 5).
G -> E (IN REF. 3).
G -> E (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-F1B; TISSUE-Skeletal muscle; MEDLINE-95278335; PubMed-7758576; Roberds S.L., Campbell K.P.;
                                                                                                                                                                                                                                                                                                                                                                                                              Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: HEART MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                LVEH 235
                                                                                                                                                                                                          GGLWRL------VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVT----
                                                                                                                                                                                                                                                TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC
                                                                                                         GILEHDPFFCPPTEATGRDFLADALVTLLVPLLVALLL---TLLLAYIMCCRREGQLKRD
                                                                                                                                                CAQGQPPLLSCYDSLAPHFRVDWCNVSLVDKSVPEPLD----
                                                                                                                                                                    CAFQPPP--SC-----LRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPD 161
                                                                                                                                                                                       GGLWELGELQLLNITSALDRGGRVPLPIEGRKEGVYIKVGSATPFSTCLKMVASPDSYAR
                                                                                                                                                                                                                             TTRQRLLLLI-----EDPEGPRLPYQAEFLVRSHDVEEVL----PSTPANRFL--TAL
                                                                                                                                                                                                                                                                                                                                                                                                                      D83651;
U21677;
                                                                   MATSDIQMVHHCTIHGNTEELRQMAARREVPRPLSTLPMFNVRTGERLPPRVDSAQVPLI
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                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  requires a license agreement (S
an email to license@isb-sib.ch).
                               387
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                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                     BAA12025.1;
AAA81645.1;
                                                                                                                                                                                                                                                                                                                      AA,
                                                                                                                                                                                                                                                                                                                                         23
387
290
311
387
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                                                                                      ·LHWQRTRRRTPRP-----
                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

CYS-RICH.

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                            APTAPOPPLLLLLLPVGLLLLAAAWC
                                                                                                                                                                                                                                                                             Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Signal. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                          ALPHA-SARCOGLYCAN
                                                                                                                                                                                                                                                                                                                     -LINKED (GLCNAC. . .) (P-LINKED (GLCNAC. . .) (P D8599C0FAF646C3F CRC64;
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                normal in
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                     97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the cardiomyopathic
                                                                                                                                                                                                                                                                                       Length 387
                                                                                      -GEQVPP-VPSPQ-DLL
                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                     110;
                                                                                                                                                EVPTPGD
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the
                                              REPEAT
REPEAT
                                                                                                                                               EMBL;
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_HUMAN
S3A1_HUMAN
Q15459;
Q1-NOV-1997
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DOMAIN
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MEDLINE=96079958; PubMed=7489498;

MEDLINE=96079958; PubMed=7489498;

Kraemer A., Mulhauser F., Wersig C., Groning K., Bilbe G.;

"Mammalian splicing factor SF3a120 represents a new member SURP family of proteins and is homologous to the essential factor PRP31p of Saccharomyces cerevisiae.";

factor PRP31p of Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
splicing factor 3 subunit 1 (spliceosome associated protein 114)
                                                                                                                                                    Pfam; PF01805; Surp; 2. Pfam; PF00240; ubiquitin; 1. SMART; SM00213; UBQ; 1.
                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114) (SF3A120).
SF3A1 OR SAP114.
                                                                                                                                                                                                    InterPro; IPR000061; Surp. InterPro; IPR000626; Ubiquitin.
                                                                                                                                                                                                                                            MIM; 605595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional association (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Das R., Zhou Z., Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10882114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bentley D., Blandford Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Bentley D., Blandford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTS WITH SF3A3
                                                                                                                                                                                                                                                                           x85237;
                                                                                                                                                                                                                                                           X85237; CAA59494.1; -. AC004997; AAC23435.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa;
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                                                                                                                   processing;
                                                                                                                                     UBIQUITIN_2; 1
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SURP MOTIF 2.
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            POLY-GLN.
POLY-GLU.
                                                               UBIQUITIN-LIKE
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Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                     Nuclear protein; Repeat.
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     TNRC_MOUSE
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Best Local
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTBR OK INCL.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata;

Eukaryota; Fiitheria; Rodentia;
                                                 between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                  sequence trap and chromosomal mapping.";
Genomics 30:312-319(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OV-1997 (Rel. 35, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
        entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                Browning J.L., Ware C.F.; "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding, and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CVB; TISSUE-Lung;
MEDLINE-96072804; PubMed-7594541;
Force W.R., Walter B.N., Hession
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=96163885; PubMed=8586432;
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                         Honjo T.;
"The murine lymphotoxin-beta receptor
                                                                                                                                                                                                                                                                                            Nakamura T., Tashiro
                                                                                                                                                                                                                                                                                                                                                                  J. Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                         SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                          FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE IMMUNE DEVELOPMENT.
                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
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22.3%;
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Pred. No. 4.6;
84; Mismatches
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                                                                                                     of Bioinformatics and the
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                                   (See http://www.isb-sib.ch/announce/
                                                                   There are no restrictions ng as its content is in
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                                                                                   Drosophila me
Eukaryota; Me
Pterygota; Ne
Ephydroidea;
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EMBL; L38423; AAB00846.1;
EMBL; U30798; AAA81334.1;
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                 MEDLINE=89195217;
                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:104875;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
                                                                                                                                                                                                                                                                                                                                                                236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  P--RARCQPHTRC----EIQGLVEAAPGTSYSDTICKNPPEPGAMLLLAILLSLVLFLL
                                                                                                                                                                                                                                                                                                                                                                FTTVLACAWMRHPSLCRKLGTLLKRHPE-GEESPPCPAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCLELQCQPDSSTLPPPWSPRPLEATAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECRCQPGMSCVYLDNECVHCEEERLVLCQPGTEAEVTDEIMDTDVNCVPCKPGHFQNTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00208; TNFR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  -LAAAWCLHWQRTR-----RRTPRPGEQVPPVPSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                 melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musca; Drosophilidae; Drosophila.
 O'Farrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFR_c6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ltbr.
                   PubMed=2702688
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72
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POTENTIAL
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TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 87.5;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR-CYS
                                                                                                                                                                                       update)
.48) (STRING
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                                                                                                     Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                  274
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                                                                                                                                                                                         PROTEIN) (CDC25-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
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Gaps

8

235 198 182

FlyBase; FBgn0003525;

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RX MEDILINE-2019606; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Asburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Harndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Harli J.F., Agbayani A., And H.-J., Andrews Pfannkoch C.R., Miklos G.L.G.,
RA Harli J.F., Agbayani R.A., And H.-J., Andrews Pfannkoch C.B., Blatkin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,
Ra Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Doubon K. Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W.,
Rosler C., Gabratlain A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Doubon K.D., Beli Y., Levisky A.A., Li J., Hernandez J.R., Bouck J.,
RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Bouck J.,
RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Bouck J.,
RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Bouck J.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Kenrica S., Fleischmann W.,
Rosland B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., Wolferd M.P., Herris M.,
RA Harris M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Harris M., Now M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Harris M., Wolfer R., Fereige G., Wolfer F., Scheeler F., Shen H.,
RA Menn L., Sheng L., Saveti J.S., Scheeler F., Shen H.,
RA Mann L., Sheng L., Wolfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-91006056; PubMed-2120044;
Jimenez J., Alphey L., Nurse P., Glover D.M.;
Jimenez J., Alphey L., Nurse P., Glover D.M.;
Jimenez J., Alphey L., Nurse P., Glover D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genetic control of cell division patterns Cell 57:177-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complementation of fission yeast cdc2ts and cdc25ts mutants identifies two cell cycle genes from Drosophila: a cdc2 homologue and
                                                                                                                                                                                                                                                                    SIMILARITY: STRONG,
                                                                                                                                                                                                                                              AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                       PROTEIN TYROSINE + ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                  TO OTHER SPECIES M-PHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
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                                                                                                                                                                                                                                                                  INDUCER PHOSPHATASE
                                                                                                                                                                  restrictions
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EMBL; M24909; AAA28916.1; -. EMBL; X57495; CAA40732.1; -. AE003768;

Вb δÃ Ş 밁 γQ 맑 δõ В DЬ Q DDR1_RAT RESULT Query Match Best Local Matches DDR1_RAT Q63474; Q63474; Q1-NOV-1997 Q1-NOV-1997 20-AUG-2011 Sanchez M.P., Tapley P., Saini S.S., "Multiple tyrosine protein kinases ir isolation of Ptk-3, a receptor expres the developing brain";
Proc. Natl. Acad. Sci. U.S.A. 91:1815 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 45, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EPITHBLIAL DISCOIDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112)
(TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE)
DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (PROTEIN-TYROSINE KINASE SEQUENCE 479 AA; 54094 MW; 684

SMART; SM00450; RHOD; 1.

Cell division; Mitosis; Hydrolase.

BY S1

BY S1

CONFLICT 228 228 A ->

SEQUENCE 479 AA; 54094 MW; 684 STRAIN-SPRAGUE-DAWLEY; TISSUE-Bra MEDLINE-94173920; PubMed-8127887; Eukaryota; Metazoa; Mammalia; Eutheria: InterPro; IPR000751; MPI_Phophtase.
InterPro; IPR0001763; Rhodanese_domain.
Pfam; PF00581; Rhodanese; 1.
PRINTS; PR00716; MPIPHPHTASE. HSSP; P30304; 1C25 FlyBase. T SEQUENCE FROM NCBI_TaxID=10116; [1] -Rattus norvegicus 243 174 147 118 118 200 58 72 RECOGNITION MAY DE ALL PROTEIN TYROSINE - ADP +
RECOGNITION (BY SIMILARITY).

RECOGNITION (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO
PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.

PROLIFERATIVE AUTH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN ب 9 OR EDDR1 OR PTK3 VTISH CSMESSMDDE-----YMELFEMESQSQ-----QTALGF----MGLLSPEGSPQRFQIVRQPKILPAMGVSS------DHTPARS-FRI-FNSLSS-----T 117 MTVLAPAWSPTTYLLL----LLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYP LLVEH SCLREVQTNISRLLQETSEQLVALKP---WITRQNESRCLEL-QCQPDSSTLPPPWSPRP VTVASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP 117 LEATAPTA---PQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDL SGLN----TARDCFKRPEPP--Similarity Eutheria; Conservative N.A. SLISGQIKEQPAAKSPAGLSMRRPSVRRCLSMTESNTNSTTTPPPKTPE-STANDARD; (Rat) Chordata; Rodentia; 7 22 TISSUE-Brain; . 0%; 34; BY SIMILARITY A -> T (IN RE Pred. No. 3.4 4; Mismatches Score Craniata; Vertebrata; Sciurognathi; Muridae 91:1819-1823(1994). IN CELL-CELL INTERACTIONS S.S., He B., Pulido D., Barbaci ases in rat hippocampal neurons expressed in proliferative zone -> T (IN REF. 1) 68483F3A285962CC NO. **ASANCSPIOSKRHRCAAVEKENCPAPSPLSQ** 7.5; 910 В Muridae; 76; CRC64; Length 479; Indels Euteleostomi; Barbacid zones 79; ----p Rattus KINASE Ξ :. Gaps of 242 57 230 173 14;

DDR1_MOUSE Q03146; Q1-OCT-1994 Q1-NOV-1997 20-AUG-2001

(Rel

Created)

STANDARD;

PRT;

911

01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112)
TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE
DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (PROTEIN-TYROSINE KINASE

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; Sciurognathi; Muridae;

Euteleostomi;
; Murinae; Mus

NCBI_TaxID=10090;

MPK-6). DDR1 OR EDDR1 OR CAK OR MPK6

Mus musculus

(Mouse)

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RESULT 10
DDR1_MOUSE
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Best Local
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CARBOHYD
CARBOHYD
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ACT_SITE
DISULFID
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MOD_RES
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
NP_BIND
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SMART; SM00231; FA58C; 1.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00109; PROFEIN_KINASE_TYR; 1

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; PROSITE; PS01285; FA58C_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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SIGNAL 1
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PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                     143
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SIMILARITY:
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een the Swiss Institute of Bioi
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P11362; 1FGI.
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Tyrosine-protein kinase: Glycoprotein; Signal;
ion: Transmembrane; Receptor; ATP-binding.
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Gilardi-Hebenstreit P., Nieto M.A., Frain M., Mat Chestier A., Wilkinson D.G., Charnay P.; "An Eph-related receptor protein tyrosine kinase

STRAIN=C57BL; TISSUE=Embryonic br MEDLINE=93096484; PubMed=1281307;

brain;

Mattei

м. -G

gene segmentally

SEQUENCE OF 766-822 FROM N.A

expressed in the developing mouse hindbrain."; Oncogene 7:2499-2506(1992).
-!- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS

RECOGNITION (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE =
PROTEIN TYROSINE PHOSPHATE.

ADP

SUBCELLULAR LOCATION: TYPE I MEMBRANE ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK

PROTEIN.

HERE) AND CAK II; Y DIFFER BY THE

EXPRESSED

IN VARIOUS

-

coexpressed in breast tumor cell lines oncogene 12:1469-1477(1996).

Perez J.L., Jing S.Q., Wong T.W.; "Identification of two isoforms of the

Cak receptor kinase that .";

MEDLINE=96204002; STRAIN-C57BL SEQUENCE FROM N.A.,

PubMed=8622863;

AND

ALTERNATIVE

SPLICING

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PROSITE;
PROSITE;
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PROSITE;
                                                                                    SMART;
SMART;
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HSSP; P11362; 1FGI.
MGD; MGI:99216; Ddr1
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                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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- SIMILARITY: CONTAINS 1
- SIMILARITY: BELONGS TO PROTEIN KINASES.
p: MGI:99216; Ddr1.

cerpro; IPR000719; Euk_pkinase.

cerpro; IPR000421; FA58_C.

cerpro; IPR000421; FA58_C.

cerpro; IPR001245; Tyr_kin.

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cerpro; IRR1; SM00231; FA58C; 1.

cerpro; IRR1; IR
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TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS IDEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED EPITHELIAL CELLS.
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X57240; CAA40516.
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Best Local S
Matches 38
Koerschen H.G., Illing M., Seifert R., Se Gotzes S., Colville C., Mueller F., Dose Kaupp U.B., Molday R.S.;

"A 240 kDa protein repressional control of the 
                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; C
Mammaila; Eutheria; C
Bovidae; Bovinae; Bos
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                          CNG4_BOVIN STANDARD; PRT; 1394 AA.

Q28181; Q28082; Q03861;

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

20-AUG-2001 (Rel. 40, Last annotation update)

240 KDA PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL (CONTAINS: GLUTAMIC ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4

(CNG CHANNEL 4) (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
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                photoreceptor.";
                                complete beta subunit
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Dose A.,
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tor; ATP-binding;
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                                 of the cyclic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biel M., Zong X., Ludwig A., Sautter A., "Molecular cloning and expression of the cyclic nucleotide-gated cation channel."; J., Biol. Chem. 271:6349-6355(1996).
                                                                                                                                                                                                                                                                                        InterPro; IPR002025; CNG_membrane.
InterPro; IPR000595; CNMP_binding.
Pfam; PF00914; CNG_membrane; 1.
Pfam; PF00027; CNMP_binding; 1.
                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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[2]
        CONFLICT
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X94707;
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CAA64367.1;
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A -> T (IN REF. 3).
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R (IN REF. 3).
S -> A (IN REF. 2).
R -> A (IN REF. 2).
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R -> Q (IN REF.
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CONFLICT
SEQUENCE
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                                                                                                                                                         EMBL;
                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                 SEQUENCE
                                                                                                                                     Glycoprotein;
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01-OCT-1996 (Rel. 34, Last annotation update)
SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-F. NAGARIENSIS / HK10;
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160 PDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGE 219
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e extracellular matrix of Volvox carteri: molecular structure
cellular compartment.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 161-282 FROM N.A.

MEDITINE-99303793; PubMed-1037350;

MEDITINE-99303793; PubMed-1037350;

Pati D., Meistrich M.L., Plon S.E.;

"Human Cdc34 and Rad6B ubiquitin-conjugating enzymes target repressors of cyclic AMP-induced transcription for proteolysis.";

of cyclic AMP-induced transcription for proteolysis.";

nol. Cell. Biol. 19:5001-5013(1999).

i- PUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)

(CONSENSUS: 5'GTGACGT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN MANY

VIRAL AND CELLULAR PROMOTERS.
                                                                                                                                                                                                                                                                                     EMBL; AF305687; AAG22558.1; -.
EMBL; AF021663; BAA78477.2; -.
EMBL; AF101388; AAD28370.1; -.
EMBL; AF101388; AAD28370.1; -.
InterPro; IPR002537; Ham1p_like.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR001871; bZIP.
                                                                                                                                                               PROSITE; PS00036;
                                                                                                                                                                                                           Pfam; PF00170; bZIP; 1.
PRINTS; PR01217; PRICHEXTENSN.
ProDom; PD004952; Ham1p_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified
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Kohroki J., Tanaka
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Emson P.C., Billinton A., Marshall F.H.;
"The GABAB receptor interacts directly with the related
factors CREB2 and ATFX.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                           Multigene
                                                                                                                                 Transcription regulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). SIMILARITY: TO OTHER BZIP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: BINDS DNA AS A DIMER (POTENTIAL). INTERACTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long as its content and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Tanaka K.; (DEC-1998) t
                                                                                                        family
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186
210
236
                                                                                                                                                                                     2; Ham1p_like; 1.
BRLZ; 1.
                                                                                                                                                               BZIP_BASIC;
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194
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250
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Primates;
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                                                                                                                              SIC; 1.
DNA-binding;
BASIC MOTIF.
LEUCINE-ZIPPER (PROBABLE).
                                                      POLY-PRO
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                                                                                                                                   Activator;
                                                                                                                                   Nuclear
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Best Local
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TECEPICI. ;
STRUCTURE 6:63-73(1998).

STRUCTURE 6:63-73(1998).

-I- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS GAMMA. MEDILATES THE SELECTIVE UPPRAKE OF TIGE FROM MILK AND HELDS NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY: IGG IN THE MILK IS BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE RESULTANT FCRN-TGG COMPLEXES ARE TRANSCYTOSED ACROSS THE INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCRN INTO BLOOD (TISSUE FLUIDS (BY SIMILARITY).

-I- SUBUNIT: FCRN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH AND THE PARTY OF TWO SUBUNITS: P51, AND P14 WHICH AND THE PARTY OF TWO SUBUNITS: P51, AND P14 WHICH AND THE PARTY OF TWO SUBUNITS: P51, AND P14 WHICH AND THE PARTY OF TWO SUBUNITS: P51, AND P14 WHICH AND P14 WHICH AND P15 WHICH AND P15 WHICH AND P15 WHICH AND P15 WHICH AND P16 WHICH AND P17 WHICH AND P17 WHICH AND P18 WHIC
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SEQUENCE
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01-JAN-1990 (Rel. 1
15-JUL-1998 (Rel. 3
IGG RECEPTOR FCRN I
RECEPTOR) (IGG FC F
                                                                                                                                                                                                                                                                                                                                             MEDLINE=95059482; PubMed=/yuyyyu, Burmeister W.P., Huber A.H., Bjorkman P.J.;
"Crystal structure of the complex of rat neonatal Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FCGN_RAT P13599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and expression of the neonatal rat intestinal Fc receptor, major histocompatibility complex class I antigen homolog."; Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
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MEDLINE=90315866; PubMed=2534798;
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STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae,
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                         MEDLINE-98154319;
                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 337:184-187(1989).
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FCGRT OR FCRN.
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01-JAN-1990
                                                                                                                                                                                                                   receptor."
                                                                                                                                                                                                                                                          Vaughn D.E.,
                                                                                                                                                                                                                                                                                                                                    Nature 372:379-383(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simister N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simister N.E., Mostov K.E
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                                                                                                                                                                                                                                    "Structural basis
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282
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36, Last annotation update)
LARGE SUBUNIT PSI PRECURSOR (FCRN) (NEONATAL
FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN).
                                                                                                                                                                                                                                of pH-dependent antibody binding by the neonatal
                                                                                                                                                                                                                                                                             PubMed=9493268;
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Pred. No. 3;
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                                  AND P14 WHICH
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            MNT_HUMAN
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DOMAIN
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EMBL; M35495; AAA41611.1; -.
EMBL; S02117; S02117.
PIR; S0217; A37374.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR001220; Lecttin_legB.
InterPro; IPR001039; MHC_I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1FRT; 14-FEB-95.
3FRU; 10-JUN-98.
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                                     LLLLA---
                                                                               GDGSFHAWSLLEVKRGDEHHYQCQVEHEGLAQPLT--
LLLVVVAIAGGVLLWNRMRSGLPAPWLSLSGDDSGDLLPGGNLPPEAEPQ
                                                                                                                                                                  -----TCAAFSFYPPELKFRFLRNGLA-------SGSGNCSTGPN
                                                                                                                                                                                                          NTEIHFVTKCA----FQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRC-----
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n; IG
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Pred. No.
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1; Mismatches
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(POTENTIAL).
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(Rel. 37, Created)

STANDARD;

PRT;

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Best Local
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11- FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES
TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE
5'-CACGTG-3' AND, WITH HIGHER AFFINITY, TO 5'-CACGCG-3'.

SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX.

-1- SUBCELLULAR LOCATION: NUCLEAR.

-1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998
20-AUG-2001
MAX BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97327566; PubMed=9184233;
Meroni G., Reymond A., Alcalay M., Borsani G., Tanigami A.,
Tonlorenzi R., Lo Nigro C., Messali S., Zollo M., Ledbetter D.H.
Brent R., Ballabio A., Carrozzo R.;
"Rox, a novel bH.HZip protein expressed in quiescent cells that
heterodimerizes with Max, binds a non-canonical E box and acts a
transcriptional repressor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nigro C.L., Venesio T., Reymond A., Cainarca S., Enrico F., Stack M., L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                    Transcription regulation;
                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                   Pfam; PF00010; HLH;
                                                                                                                                                                                                                                                                                                InterPro; IPR003015;
InterPro; IPR001092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 16:2892-2906(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The human ROX Gene: genomic structure and mutation analysis in
                              186 LAPQQPPPPTLGTLKLAPAEEVKSSEQKKRPGGIGTREV---HNKLEKNRRAHLKECFET
52 £LQDY?VTVASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKC 111
                                                                                                              Local Similarity
                                                               4 LAPAWSPTTYLLLLLLSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                            X96401; CAA65265.1;

X13440; CAA73851.1;

X13442; CAA73851.1;

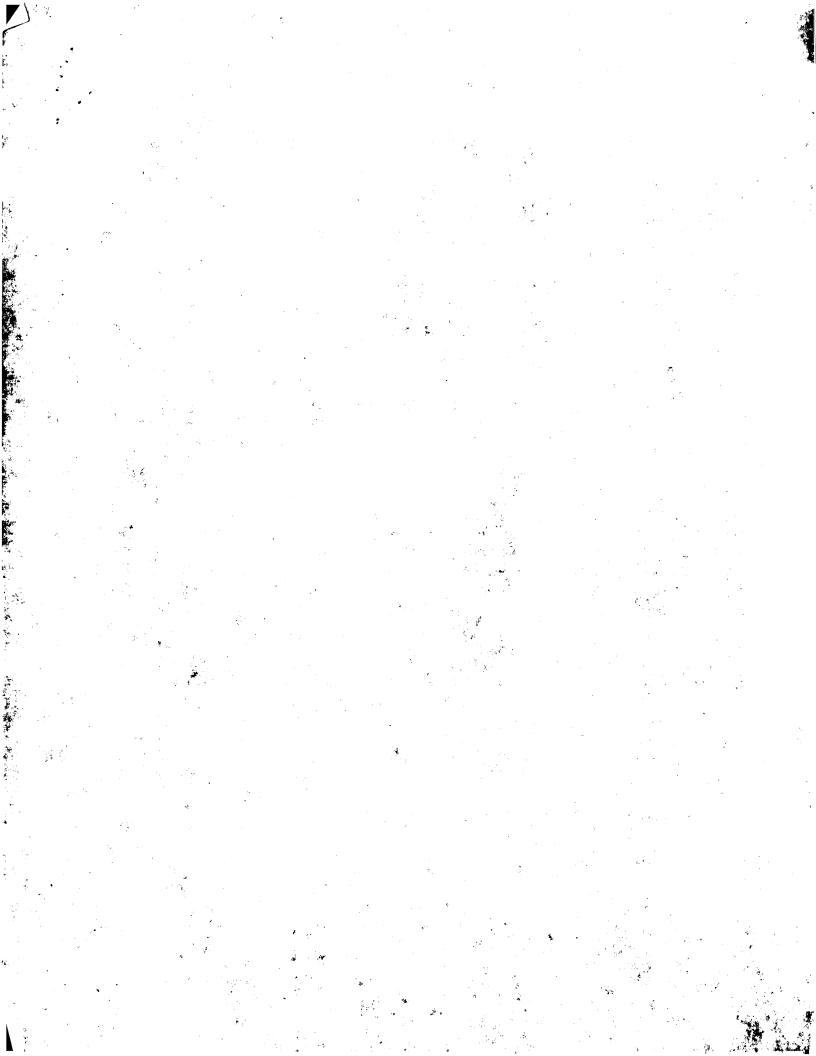
X13442; CAA73851.1;

X13443; CAA73851.1;

X13443; CAA73851.1;
                                                                                                                                                                                                                                                                                                                                               Y13444; CAA73851.1;
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(Rel. 40, Last annotation update)
PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT).
                                                                                              Conservative
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; Primates;
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21.1%;
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HLH_dim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          institutions as long
                                                                                                                                                                Repressor: Nuclear protein; DNA-DINGLIN
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (POTENTIAL).
LEUCINE-ZIPPER.
MW; 06AC320D79BF18A0 CRC64;
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JOINED.
JOINED.
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                                                                                                            Score 84; DB 1; Pred. No. 8.5;
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                                                                                              Mismatches
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Ledbetter D.H., Liscia
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i S., Zollo M., Ledbetter D.H.,
                                                             -GLSGTQDCSFQHSPISSDFAVKIRELSDY 51
                                                                                                                                                                                                                                    Nuclear protein; DNA-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as its content
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                                                                                                                         Length 582;
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---PHSVALPPAHLPVQQQQPQQKTPLPAPPPPPAAPAQTLVPAPAHLV
                            LLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPP-----VPSPQDLL 231
                                                              EGEDNIDEDMEEDRAGLGPPKLSHRPQPELLKSTLPPPSTTPAPL---
                                                                                                                             A------TQQRLAELKHELSQ------WMDVLEIDRVLRQTGQPEDDQASTSTAS
                                                                                                                                                          AFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPD------
                                                                                             -----STLPPP-WSPRPLEATAPTAPQPPLLLL 189
                                                                -PPHPHPH----
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Search completed: April 1, 2002, 06:27:05 Job time: 626 sec



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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                   894.5
894.5
894.5
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Sp_archea:*

sp_bacteria

sp_bacteria

sp_fungi:*

sp_human:*

sp_inverteb

sp_mammal:*

sp_mhc:*

sp_organel:*

sp_plage:*

sp_plant:

sp_virus:

sp_virus:

sp_virus:

sp_unclas:

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1 MTVLAPAWSPTTYL
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Gapop 10.0 , Gapext 0.5
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Best Local S
Matches 182
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MEDLINE-20358731; PubMed=10902925;
Yang S., Sim G.K.;
Molecular cloning of canine and feline flt3 ligand reveals high degree of similarity to the human and mouse homologue but uniquely long cytoplasmic domain.";
DNA Seq. 11:163-166(2000).
EMBL; AF155148; AAF87088.1; -
EMBL; AF155148; AAF87088.1; -
EMBL; AF155148; AAF87088.1; -
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Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheriä; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID-9615;
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Pred. No. 6.6e-7
12; Mismatches
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Best Local Similarity 80.5
Matches 178; Conservative
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EMBL; AF282985; /
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01-OCT-2000
01-OCT-2000
                                                                                                  SEQUENCE FROM N.A.
PubMed=11120823;
Mwangi W., Brown W.C., Palmer G.H.;
"Identification of fetal liver tyrosine kinase required for receptor binding and function usin igand isoforms.";
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Cetartiodactyla; Rus Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TIEMBLIEL 16, 01-MAR-2001 (TIEMBLIEL 16, 01-MAR-2001 (TIEMBLIEL 16, FLT3 LIGAND ISOFORM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degree of similarity to the human and mouse homologue but uniquely long cytoplasmic domain.";
DNA Seq. 11:163-166(2000).
EMBL; AF155149; AAF87089.1;
SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DCC6 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
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                                     165:6966-6974(2000).
985; AAF99322.1; -.
292 AA; 32390 MW; D
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Pred. No. 8.1e-77;
9; Mismatches 33
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Felis.
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                                                                                                                                                                                                                                                                                          Bovoidea;
                                                                                                                          occurring
                                                                                                                                               domain
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RESULT
Q61104
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PRESIDENT PRESIDENT OF THE PRESIDENT OF 
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Best Local
Matches 15
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Best Local Sin
Matches 171;
Q61104
Q61104;
01-NOV-1996
01-NOV-1996
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01-MAR-2001
01-MAR-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

PubMed=11120823;

Mwangi W., Brown W.C., Palmer G.H.;

Midentification of fetal liver tyrosine kinase 3

required for receptor binding and function using
ligand isoforms.";
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Q9GKD9;
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ONIENCE 274 AA; 30372 MW;
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AR-2001 (TrEMBLrel. 16,
AR-2001 (TrEMBLrel. 16,
LIGAND ISOFORM-2.
                                                                                                                                                                                                            PGPQSPLLLLLLLLPVALLLLATAWCLCRWRRRRRTRYPGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTVLAPAMSPTT-YLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAPQPP----LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQ
                                                                                                                                                                                                                                                                                                                                           LRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGPQSPLLLLLLLLLPVALLLLATAWCLCRWRRRRTRYPGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156;
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                                                                              PRELIMINARY;
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76.3%; Pred. No. 1.2
Live 12; Mismatches
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Last sequence up
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Pred. No. 8.6e-63
2; Mismatches 3
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No. 1.2e-71;
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(TrEMBLrel.

01, 01,

Created) Last sequence

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RESULT
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Best Local S
Matches 122
                                                                                                                                                                                                                                                                                                              Q9LGG8 PRELIMINARY; PRT;
Q9LGG8;
01-OCT-2000 (TrEMBLrel. 15, Created
01-OCT-2001 (TrEMBLrel. 17, Last sc
01-JUN-2001 (TrEMBLrel. 17, Last ar
PUTATIVE EXTENSIN-LIKE PROTEIN.
P0406H10.6 OR OJ1174_D05.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McClanahan T., Culpepper J., C
Mattson J., Tsai S., Luh J., G
Birnbaum D., Hannum C.;
Submitted (DEC-1995) to the EM
EMBL; U44024; AAA93305.1; -.
MCD: MCI:95560; Flt31.
                                                                                                                                                                                                   STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamar
"Oryza sativa nipponbare(GA3)
clone:P0406H10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JGN-2000 (TrEMBLrel.
PRINTS; PRO1217; PRICHEXTENSN. SMART; SM00370; LRR; 5. PROSITE; PS00030; RRM_RNP_1; U
                                                                                    Submitted (JAN-2001) to the EMEMBL; AP002524; BAB07956.1; -. EMBL; AP003118; BAB33013.1; -.
                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnollophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                          InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR.out.
InterPro; IPR002565; P_rich_extensn
InterPro; IPR000504; RRM.
                                                                                                                     "Oryza sativa nipponbare(GA3) clone:OJ1174_D05.";
                                                                                                                                          STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                clone: P0406H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                      (JUN-2000)
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 RRM_RNP_1; UNKNOWN_1.
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72.6%;
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                                                                                                                                          Yamamoto
                                                                                                                                                                                                                      Yamamoto
                                                                                                                                                                                                                                                                                  Streptophyta; E
yta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last
                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                     EMBL/GenBank/DDBJ
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Guimares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 602.5; DE Pred. No. 2e-49;
                                                                                                                                                                                                        moto K.;
genomic
                                                                                                                               genomic
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04F0A010171E3384 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                               DNA,
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                                                                                                                                                                                                                                                                                   Embryophyta; Trach
a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                    AA
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                                                                                                                               chromosome
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Best Local S
Matches 54
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=MAASTRICHT;
MEDLINE=20366325; PubMed=10906222;
MEDLINE=2036625; PubMed=10906225; PubMed=10906225; PubMed=10906225; PubMed=10906225; PubMed=10906225; PubMed=1090625; PubMed=109065; PubMed=1090625; PubMed=1090625; Pu
Q9C5T0;
                                                                                                               1113
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STRAIN-MASCIRICHT;
MEDLINE-20473137; PubMed-11018281;
Gruijthuijsen Y.K., Beuken E., Bruggeman
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01-MAR-2001
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NCBI_TaxID=79700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat cytomegalovirus (st. Viruses; dsDNA viruses,
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                                                                                                                                                   AWCLHWQRTRRRTPRPGEQVPPVPSPQD
                                                                                                                                                                                                                           PDSSTL---
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                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                             -QATRASPRPETDAPP-PTPAD
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                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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uses, no RNA stage; H
Muromegalovirus
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33.0%;
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23.78;
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16,
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Last sequence up
                                                                                                                                                                                                                                                               Score 95.5; D
Pred. No. 1.7;
8; Mismatches
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Pred.
                   PRT;
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No. 0.
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which
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Best Local
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InterPro; IPR001245; Tyr_kin.
Pfam; PF01657; DuF26; 1.
Pfam; PF00069; pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                     O17889;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TREMBLrel. 05, Last sequence update)
O1-JUN-2001 (TREMBLrel. 17, Last annotation updat
FEAF12.1 PROTEIN (EC 3.1.3.48).
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton Gardner A. Green P., Hawkins T., Hillier L., Jier M., Joh
                                                                                            SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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Submitted (JAN-2000) to the
EMBL; AF224705; AAK28315.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
RECEPTOR-LIKE PROTEIN KI
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Du L., Chen Z.;
                                                                                                                                                                                                                                                              NCBI_TaxID=6239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Kinase; Transferase.
SEQUENCE 658 AA; 72991 MW; DC
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InterPro; IPR000719;
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                                                                                                                                                                                                                                                                                 Nematoda; Chromadorea; cinae; Caenorhabditis.
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25.8%;
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Euk_pkinase.
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Last
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Pred. No. 1.3;
16; Mismatches
                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
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edons; core eudicots; Rosic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
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                                                                                                                                                                 databases
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WRKY DNA-bindin
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                                                 Coulson
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Best Local
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Best Local
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    Matches
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Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownk
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III o
                                                                                                                                                                                   PROTEIN MP-2 r...
Homo sapiens (Human).
Homo sapiens (Human).
'harvota; Metazoa; Chordata;
'harvota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HAD2;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ11798 FIS, CLONE HEMBA1006198, WEAKLY SIMILAR TO PROLINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00102; Y_phosphatase; 1.

SMART; SM00194; PTPC; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_1; 1

PROSITE; PS50056; TYR_PHOSPHATASE_2; 1

PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HAD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z81548; CAB04464.1; -.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase
                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPVGLLLLAA----AWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MERLKTVAGSKMQGL---LERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALRPOPTTSDPTAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALKPWITRONFSRCLELQCQPDSSTL - - - PPPWSPRPLEATAPTAP - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                          pR01217; PRICHEXTENSN.
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                         AA;
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                                                                                                                         26607
                        7.48;
31.98;
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                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
Score 92; DB 4; Pred. No. 0.64; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 93; DB 5
Pred. No. 2.8;
33; Mismatches
    9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                         420195B27966FD41 CRC64
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    39;
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                                           Length
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
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    46;
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    Gaps
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115

PPPSCLREVQTNIS-----

RLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPW

RESULT Q9PU36

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Query Match
Best Local Similarity
Matches 45; Conser
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Pfam; PF001595; PDZ; 1.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00239; C2: 2.
SMART; SM00239; C2: 2.
SMART; SM00239; C2: 2.
SMART; SM00239; C2: 2.
PROSITE: PS00499; C2_DOMAIN_1; U1
PROSITE: PS00499; C2_DOMAIN_2; 2.
PROSITE: PS0106; PDZ; 1.
NON_TER 1
NON_TER 1
NON_TER 5120 AA; 560760 MW;
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09PU36; PTEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zones, shares homology profilin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae;
                                                            2344
                                                                                                                                                                                                                    2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001478; PDZ.
InterPro; IPR002965; P_rich_extensn
InterPro; IPR001565; Synaptotagmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Cell Biol. 147:151-162(1999).
EMBL; Y19187; CAB60725.1; -.
HSSP; P04410; 1A25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang X., Kibschull M., Laue
Kilimann M.W.;
"Aczonin, a 550-kd putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99439764; PubMed-10508862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACZONIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000008; C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128
                                                                                                                                                                              127
                          222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPRPLPQALVPPQDHPGSSPRTTQAPPLL--
                                                                                                                                                                                                                AARKMKSTVETGIIKIHHEDSHKELSLDMTRINLTGATSEQPPLCVASVSVKEPASETPA
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                        PPVPS
                                                                                                                                     VPTPRVVSKTSTVSMPSSAPALTSKVFSLFRSSSLDSPAQPSPPSPPPPPPPPPPPPPPPPP
                                                                                                                                                                          --ISRLLQETSE-QLVALKPWITRQNF----SRCLELQCQPDSSTLPPPWSPRPLEATAP
                                                                                                                                                                                                                                                     AGSKMQGLLERVNTEIHF-------VTKCAFQPPPSCLRFVQTN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPRPL-EATAP-----
                                                          ILPKPAIYPKKKSQIQAPMATAPTAVPLVTSVATLESAAVLKNHVVPVTKTYTPTP-PPV
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                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                7.3%;
                                                                                                                                                                                                                                                                                                                                                                                           560760 MW;
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                                                                                               -PLLLLLLPVGLLLLAAAWCLH-WQRTRRRTPRPGEQV
                                                                                                                                                                                                                                                                                             19;
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ons with rim
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Last sequence update)
                                                                                                                                                                                                                                                                                         Score 90.5; DI Pred. No. 22; .9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                           A658D9891B65B412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lichte
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                                                                                                                                                                                                                                                                                                                                    DΒ
                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                             72;
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                                                                                                                                                                                                                                                                                                                                Length 5120
                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                             Indels
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n and binds
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                                                                                                                                                                                                                                                                                             49;
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                                                                                                                                                                                                                                                                                           Gaps
                                                          2402
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                                                                                                                                                                          179
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                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Q9UMT1
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017610
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Submitted (NOV-1996) to the Emm.,
Submitted (NOV-1996) to the Emm.,
EMBL; Z82259; CABO5129-1; -.
EMBL; Z82259; -.
EMBL
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017610;
01-JAN-1998
                  Cantoni C., Biassoni R.;
"NKP44 related genes.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                     O9UMT1;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                               SEQUENCE FROM N.A. TISSUE-LYMPHOID;
                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Rhabditidae; Pelode:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Caenorhabditis elegans.
Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C28D4.2 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999
01-JUN-2001
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                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFTLLSERNLGPKMLGVFPGGRFEQFIPSRALQCLEISKPGLSKLIAPIVARVHTLDAPI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKIEEF -- RIRAITGG - MSNLLFLVELPAH - LTPIQMEPEKALLRVHCQSDIDQLLSESV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLR-FVQTNISRLLQET- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKEPQ
AJ010100; CAB52290.1;
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59; Conserv
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24.18;
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17,
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Last
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Pred. No. 2.2;
29; Mismatches
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                                                                                                                                                                                            Craniata; Vo
Catarrhini;
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annotation update)
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on update)
                                                                                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -OPDSSTLPPPWSPR--PLEATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
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                                                                                                                                                                                                              Euteleostomi;
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Best Local S
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Pfam; PP00047; Ig; 1.
SMART; SM00409; IG; 1
SEQUENCE 270 AA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
P0489A05.3 PROTEIN.
P0489A05.3.
                                                                                                                                                                                                                                                  Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003105; BAB32983.1; -. SEQUENCE 404 AA; 43109 MW; 7CA66FDE7772A64B CRC64;
                                                                                                                                                                                                                                                                                             STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
**ROTYZa sativa nipponbare(GA3) genomic DNA,
clone:P0489A05.**;
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9AWJ4
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157
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   221
                           131 LOETSEQLVALKPWITRQNFSR----CLELQ--CQPDSSTLP------PPWSPRPLEAT 177
                                                                                                                     107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 -LLAAAWCLHWQRTRRRTPRPGEQV--PPVPSPQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                           163
                                                                                                                                               33 QHSPISSDF--AVKIRELSDYLLQDYPVTVASNL------QDEELCGGLWRLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 ----GSLYEKKGWCKEASALVCIRLVTSSKPRTMAWTSRF-TIWDDPDAGFFTVTMTDLR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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LSATG-----TPTTTSSSILRRPLHCELLPPLRARPSPSLPLLPPLQAPPHPPLP---P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----HFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQ-CQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQD 66
                                                                                     AQRWMERLKTVAGSKMQG---LLERVNT--EIHFVTKCAFQPPPSCLRFVQTNI---SRL 130
                                                                                                                  RHSFLSFSFLEKVQITPLKYWVSMNYPLKPKNQTFFTLNYRYQMKNSPEQLCKRFW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPTAGARQAPESPSTIPVPSHPSSPLPVPLPSRPQNSTLRPGPAAPIALVPVFCGLLVAK
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                                                         -STWQSNAGAY-GSRAGGSERLLRRPSSAGRRPWLVPPPSPPPRASLAAGVPNIALTSRA
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1 Similarity 23.0%;
63; Conservative 2
                                                                                                                                                                             Conservative
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29678 MW;
                                                                                                                                                                                        7.18; 26.18;
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Ig_MHC
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                                                                                                                                                                                           Pred.
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Pred. No. 1
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Mismatches
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Best Local Similarity
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O75064;
01-NOV-1998 (TrEMB
01-NOV-1998 (TrEMB
01-JUN-2001 (TrEMB
KIAA0476 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
   1254
                                                                                                                                                                                                                                    1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of cDNA clones from human brain.";
DNA Res. 4:345-349(1997).
EMBL; AB007945; BAA32321.1; -.
                                                                                                                                                                                                                                                                                                                                                        1104 SAGASGSKDAPVPGGP-------GPVLSDRRLCLA--LDEPQLCNGHMGGASRR 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001194; DENN.
Interpro; IPR002885; PPR.
Pfam; PF01535; PPR; 1.
Pfam; PF02141; DENN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98116662; PubMed=9455484;
Seki N., Ohira M., Nagase T., Ishikawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIAA0476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330
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                                                                                                                                                                                                                                                                                                                                                                                                            SSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC----GGLWRL
                                                                                                                                                                       QLVALKPWITRONFSRCLELQCQ-PDSSTLPPPW-SPRPLEA-----TAPTAPQPP 185
                                                      LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVE 234
                                                                                                                RLPSILPGLYLAS------CDGPSHSQAPSPWLTPDPASVQVRLLWDVLTPDPNSCPP
                                                                                                                                                                                                                                    VESGAWAYLSPLVLRKELESLVENEGSEV-----LALPELPSAHPIIFWNLLWYFQRL--
                                                                                                                                                                                                                                                                                           VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPSSELLPLSRAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 08, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227
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152296 MW;
WRVHSQ-IPQRVVWPG----PVPASLSLALLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88.5; D
Pred. No. 8.6;
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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6;
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein search, using sw model
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length: 2000000000
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1242
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Gapop 10.0 , Gapext 0.5
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/SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp/AA1989, DAT: *
/SIDS2/gcgdata/geneseq/geneseqp/AA1990, DAT: *
/SIDS2/gcgdata/geneseq/geneseqp/AA1991, DAT: *
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      AAR67541
AAW67769
AAY67769
AAY60192
AAB20192
AAR66175
AAB20194
AAY69721
AAW69721
AAW69720
AAY69723
AAY69723
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224.060 Million cell updates/sec
Human flt-3 ligand
Human flt3-ligand.
Full length wild t
Human Flt-3 ligand
Human flt-3 ligand
Human flt-3 ligand
Human flt-3 mutein
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Human flt-3 mutein
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733.5	735	735	735	735	735	36	36	36	737.5	37	739	739	740.5	745	745	764	7	89	83	8	91	796.5	97	834	894.5	95	970	1100	-	$\dot{\mathbf{L}}$	1108	_	-
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19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	22	16	22	20	16	21	21	21	22	21	21	22	21	21	21	21	21	21
83		AAW69052		10	~1	m	1.1	f . 1		1.1			m	in	~1			AAB20186				AAY58207					2	6	39A	9	AAY69722	59 A	AAY69727
flt3 ligand	n flt3 ligand	t-3 recep	and FLT4C	n flt-:	flt3	eric F	n flt3	flt3	۲	n flt3	an flt-3 recep	ligano	eric rec	an fit-	ligand	e Flt-3	e MoT11	e Flt-	ne flt3	flt-3	eline mature	anine Flt-3 l	e mature	man Flt-3 liqa	e F1t-3]	ne Flt-3 l	n F1t-3 1	n flt-3 mut	n flt-3 mute	n flt-3 mute	n flt-3 mute	n flt-3 mut	Human flt-3 mutein

ALIGNMENTS

RESULT AAR67541

AAR67541 standard; Protein;

235

AΑ

05-AUG-1995 AAR67541;

(first entry)

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Key
Peptide
24-MAY-1993;
              19-MAY-1994;
                            07-DEC-1994.
                                          EP627487-A.
                                                               Domain
                                                                             Domain
                                                                                                         Domain
                                                                                                                                                   Homo sapiens
                                                                                                                                                                 Flt-3 ligand; flt3-L;
                                                                                                                                                                              Human flt-3 ligand.
                                                                                  /label- Sig_peptide
/note= "signal peptide may ext.
27..182
/label- Extracellular_domain
/note= "extracellular domain m
position 28"
9305-0068394.
              94EP-0303575
                                                     206..235
/label= Cytoplasmic_domain
                                                                             183..205
                                                                                                                                     Location/Qualifiers
                                                               /label= Transmembrane_domain
206..235
                                                                                                                                                                 anemia; cancer; AIDS; gene therapy
                                                                                                                extend
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                                                                                                               position 27"
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25-AUG-1993;
03-DEC-1993;
07-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A human T-cell lambda-gtl0 random primed cDNA library was screened with a fragment corresponding to the extracellular domain of mouse fit3 ligand (fit3-L) (nt 103-516 of AAQ79076) to isolate human fit3-L cDNA. Fit-3 stimulates progenitor and stem cells, and can be used e.g. in gene therapy protocols.
(IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                       Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L; immunogenic; autoimmune disease; organ transplantation; food aller
                                                      17-JUN-1997;
                                                                                            12-JUN-1998;
                                                                                                                                             23-DEC-1998
                                                                                                                                                                                          WO9857655-A1
                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW67769 standard; Protein; 235 AA.
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DB; AAQ79079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asnlq deelcgglwrlv lagrwmerlk tvagsk mqgller vnteihfvtk cafqpppscluder and the sum of 
                                                                                                                                                                                                                                                                                                                                                                         flt3-ligand
                                                                                                                                                                                                                                                                                  transplantation.
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93US-0111758.
93US-0162407.
94US-0209502.
94US-0243545.
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Pred. No. 3.6e-109;
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specific immune tolerance; or (ii) immunotolerance of a therapeutic
immunogenic molecule by addition of a polypeptide, before, after or with
the mucosal administration of an immunotolerising amount of the antigen
or therapeutic molecule, respectively. The polypeptide is capable of
binding the fit3 receptor and is: a) amino acids 28 x of murine fit3
ligand (fit3-I), where x is an amino acid between 160-235;
and c) a polypeptide that has at least 90% identity to the polypeptides
of either (a) or (b). The method ameliorates the effects of autoimmune
diseases, food allergies or organ or tissue rejection following
transplantation. Administration of fit3-I allows lower doses of antigens
sequence represents human flt3-I.
                                                                                           Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; fil3 ligand; fil3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
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                                                                              multiple myeloma;
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                                                                                                                                                                                                                                                                              standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the full length wild type (this sequence) or mature (AAY69720) flt3-L polypeptides. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anenia, HIV infection, breast, small cell lung, testicular or
         Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
immunotherapy; therapy; tumour; cancer; melanoma; glioma;
lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graddis TJ,
                                                                                                                                      AAB20192 standard;
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                                                           Human Flt-3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ovarian cancer,
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                                                                                                                                                                                             soluble flt3 ligand polypeptide used in cellular expansion response stimulation or treatment of pathological conditions amino acid substitutions at positions 8, 84, 118 or 122
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                                                                                                                                   Protein;
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Pred. No. 3.6e-109;
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8 or 122
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                                                                                                                                                                                                                                                 antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections;

(b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                          (Fit-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Fit-3 ligand-encoding polynucleotide, and 1 or more antigen or cytokine-encoding polynucleotides. The Fit-3 ligand-encoding polynucleotides. The Fit-3 ligand-encoding polynucleotide may encode the present full-length human Fit-3 ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, or 27-235 of the ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Fit-3 ligand and 1 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic compositions comprising Fit-3 ligand encoding polynuclectide and one or more antigen, or cytokine encoding polynuclectides, useful for suppressing tumour growth and fo autoimmune diseases (e.g. rheumatoid arthritis)
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                                                                              MTVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
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DB; AAF30310.
                            ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
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                                                                                    A cDNA library from the human stromal cell line 295V48, in pME185, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20 colones, S86 and S109, were found to be approx. 75% homologous clones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to show homology to T110 until the stop codon, although to a lesser degree, for an overall homology of 66% Clones T118 and C lesser degree, for an overall homology of 66% Clones T118 and C lesser degree, for an overall homology of a clone state on the common serious residue 163 (human residue 160). An additiona mouse c clone designated MB8 has a 29 AA insert at the junction between the common and divergent portions of the mouse ligand.
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07-JUL-1993;
16-JUL-1993;
13-AUG-1993;
24-AUG-1993;
19-NOV-1993;
03-DEC-1993;
                                                                                                                                                                                                                                                                                             New ligand for the Flt3 tyrosine kinase receptor - and related nucleic acid, vectors, host cells and antibodies, useful for treating abnormal cell physiology and proliferation, e.g. cancer, also for diagnosis and drug screening
                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            (INRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flt3 ligand; tyrosine kinase receptor ligand
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                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ79642.
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             Local Similarity
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234; Conservative
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93US-0089263.

93US-0092549.

93US-0106340.

93US-0112391.

93US-0155111.

93US-0162413.
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                                                                                polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flt-3 ligand; Fms-like tyrosine kinase;
immunotherapy; therapy; tumour; cancer;
lymphoma; autoimmune disease; infection;
         The present sequence is that of human Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3
                                                                Claim
                                                                                                                                           N-PSDB; AAF30312
                                                                                                                                                                                                                                          31-JUL-2000;
                                                                                                                                                                                                                                                                                                                     Domain
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                                                                                                                  Immunogenic compositions comprising Flt-3 ligand
                                                                                                                                                                                               (VICA-) VICAL
                                                                                                                                                                                                                    30-JUL-1999;
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                                                               2; Page 137-138; 149pp; English.
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                                                                                                                                                                                                                                                                                                                                                              /label= Signal_peptide
27..235
/label= Mature_protein
27..182
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                                                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                          /label=
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(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections;

(b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present full-length human Flt-3 ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-23 of the Flt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical
                                                                                                                                                                                                                   Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; fil3 ligand; fil3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; applastic anemia; HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein.
                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY69721 standard;
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                                              02-JUL-1998;
                                                                                                                                                                        Synthetic
                                                                                                                                                                                       Homo sapiens
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              (IMMV ) IMMUNEX CORP
                                                                            25-JUN-1999;
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                                              98US-0109100
                                                                            99WO-US14296
                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              212
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Pred. No. 1.3e-108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides CC which exhibits increased or decreased biological activity relative to the full length wild type (AAX69719) or mature (AAX69720) flt3-L CC polypeptides. This sequence represents an example of the novel flt-3 CC ligands and comprises the L-3H mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and CC binds cell surface tyrosine kinase receptors and regulate growth and CC differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or dendritic CC cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also CC modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple crowd or condition and condition or acute leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer bone marrow reconstitution; haematological disease; immune deficiency; drug-induced myelosuppression; renal dialysis; gene therapy; infection congenital metabolic disease; neurological disease; therapy;
                                                                                                                                                                                                                                                                                                       AAW69007 standard; peptide; 209
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                                                                                                production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
              'Mature wild
                                              05-มีบนั-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rearranged flt-3 receptor agonists and nucleic acids encoding them used to stimulate production of haematopoietic and dendritic cells, for treatment of haematological diseases, bone marrow reconstitution
                                                                                                            AAY69720 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                  WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                                                                                                     rqnfsrclelqcqpdsstlpppwsprpleataptapqpplllllllpvgllllaaawclh
                                                                                                                                                                                                                                                                                      RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH 206
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                human flt-3
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Pred. No. 3.6e-97;
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Best Local Similarity
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                                                                                                                           RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLLVGLLLLAAAWCLH 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAX69719) or mature (AAX69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the KB4E mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoletic progenitor cells. The flt3-L protein ca
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99.5%;
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Query Match Best Local Similarity

89.4%; 99.5%;

Score Pred.

1110; DB 21; No. 8.5e-97;

Length 209;

Sequence

209 AA;

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RESULT TARY STATE OF THE MAY 69727 ID AAYY 727 ID AAYY
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binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The fit3-L protein be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate; augment or enhance a patient's immune response and can be used to treat as immune disorder (e.g. allergy, autoimmunity or
                                                                                                                                                                                                                                           Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological condition contains amino acid substitutions at positions 8, 84, 118 or 122
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breasmall cell lung, testicular or ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia.
                                                                                                                                                                                                                                                                             Synthetic
                                            Claim
                                                                                                                                       Graddis
                                                                                                                                                           (IMMV ) IMMUNEX
                                                                                                                                                                                   02-JUL-1998;
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                                                                                                                WPI; 2000-182115/16
                                                                                                                                                                                                          25-JUN-1999;
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                                                                                                                                                                                                                                                                                          Homo
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                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                          flt-3
                                                               soluble flt3 ligand polypeptide used in cellular or response stimulation or treatment of pathological ns amino acid substitutions at positions 8, 84, 11
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08; Conservative
                                                                                                                                                                                                                                                                                                               myeloma;
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                                                                                                                                       McGrew
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                                            78-79;
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3.5e-97;
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8 or 122 -
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The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L

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RESULT
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                                                                                                                                                                                                                                                      Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                   Homo
                           Graddis TJ,
                                                                                                                                                                                                                                             multiple myeloma;
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                           McGrew JT
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                                                                                                                                                                                                                                                                           Human flt-3 mutein K84T.
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                            Issued_Patents_AA:*

1: /ggn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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US-09-109-100-10
US-08-220-379B-7
PCT-US94-05365-2
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US-08-993-962-6
US-09-160-841-6
US-09-109-100-1
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US-08-243-545-6
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Patent No. 5554512

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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ALIGNMENTS

REFERENCE/DOCKET NUMBER: 2813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS: FILING DATE: August 12, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435 APPLICATION NUMBER: US/0 FILING DATE: 11-MAY-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy FILING DATE: August CLASSIFICATION: 435
PRIOR APPLICATION DATA: ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,6 CURRENT APPLICATION DATA: APPLICATION NUMBER: US 08 FILING DATE: 03-DEC-1993 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version APPLICATION NUMBER: APPLICATION NUMBER: August 25, 1993 DN: 435 Floppy disk US 08/162,407 US/08/243,545 08/106,463 32,655 2813-C #5.1

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; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-243-545-6
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Best Local S
Matches 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
REFFRENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
_TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/06
FILLING DATE: MAY 24, 1993
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/993,962 FILING DATE: December 18, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                            ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/162,4
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
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FILING DATE: August 12,
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OPERATING SYSTEM: Macinto
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Best Local S
                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,40
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                     FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1903
APPRODRIGGY APPLICATION NUMBER: 08/068,394
                                ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 7.0.1 SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 51 Un:
CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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Reckmann, M. Patricia
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                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                32,655
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TELEFAX:

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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 235; Conserv
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SEQ ID NO 1
LENGTH: 235
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
-09-109-100-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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LENGTH: 235 amino acids
TYPE: amino acid
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             181 APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
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                                                          RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                          RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                       ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                                       ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
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Pred. No. 1.4e-117;
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RESULT 5
PCT-US94-05365-6
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      Query Match
Best Local S
Matches 235
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
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APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for
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APPLICATION NUMBER:
FILING DATE: Decembe
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APPLICATION NUMBER: -to be assigned
FILING DATE: May 11, 1994
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                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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NAME: Malas
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                                                                                        TOPOLOGY: 11
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       Local Si
hes 235;
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ZIP: 981
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                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: May 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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      similarity 100
35; Conservative
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51 University Street
                                                                                                                                235 amino acids
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1
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August 12, 1993
                                                                                                                                                                                                                                                                                                              May 24, 1993
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                   100.0%;
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7, 1994
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er 3, 1993
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                   Score 1242;
Pred. No. 1
       Mismatches
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DB 5;
1.4e-117;
0;
                                 Length
                                 235;
      0
    Gaps
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION. FLT3 L MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOSE: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 212
TYPE: PRT
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US-09-109-100-10
                                      ; ORGANISM: Homo sapiens US-09-109-100-18
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                               Sequence 18, Applicate Patent No. 6291661 GENERAL INFORMATION:
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Patent No. 6291661
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Best Local
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                                                                      TYPE: PRT
                                                                                   LENGTH: 209
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                                                                                                                                                                                                                                                                                 Application US/09109100C
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 0360 0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 209
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US-09-109-100-12
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US-09-109-100-9
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GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
                                                                                    Sequence 12, Application US/091091000 Patent No. 6291661
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Best Local Similarity
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Best Local Similarity
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Pred. No. 9.5e-105;
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Pred. No. 2
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2.4e-104;
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 209
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-109-100-12
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09109100C

Patent No. 6291661

GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03260, 0028

CURRENT APPLICATION NUMBER: US/09/109,100C

CURRENT FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 20
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SEQ ID NO 14
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 2.4e-104;
1; Mismatches 0;
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Pred. No. 2.4e-104;
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 209
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 209
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Patent No. 6291661
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Best Local Similarity
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Best Local :
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEO ID NOS: 20
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TYPE: PRT
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Pred. No. 3.8e-104;
"'omatches 0;
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Pred. No. 2.4e-104;
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CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT TILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 13
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-13
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US-09-109-100-15
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L
MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 209
     Query Match
Best Local Similarity
Matches 208; Conserv
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Best Local Similarity
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GENERAL INFORMATION:
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-TH. MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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Score 1107; DB 4;
Pred. No. 4.8e-104;
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APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09109100C Patent No. 6291661 GENERAL INFORMATION:
                                                                                                                                                                                                            Query Match 89.0%;
Best Local Similarity 99.5%;
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ORGANISM: Homo sapiens
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